

RESULT 10  
US-10-780-703-3

; Sequence 3, Application US/10780703  
; GENERAL INFORMATION:

; APPLICANT: Lee, Jong Seob  
; APPLICANT: Kim, Yun Hee  
; APPLICANT: Choi, Eun kyung  
; APPLICANT: Yoo, So Yeon  
; APPLICANT: Ahn, Ji Hoon  
; APPLICANT: Choi, Yang Do  
; TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and Method for  
; TITLE OF INVENTION: Manipulating Flowering Time of Plant Using the Same  
; FILE REFERENCE: 012679-105  
; CURRENT APPLICATION NUMBER: US/10/780,703  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: KR 10-2003-10772  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2606  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)...(2606)  
; OTHER INFORMATION: genomic DNA of LOV1 gene  
US-10-780-703-3

from  
us 10/780, 703-2.p2n.rmpm  
Seq Search Result

(Seq 3) does not  
encode Seq 2

#### Alignment Scores:

Pred. No.:	1.24e-254	Length:	2606
Score:	1735.00	Matches:	378
Percent Similarity:	43.5%	Conservative:	0
Best Local Similarity:	43.5%	Mismatches:	1
Query Match:	85.3%	Indels:	490
DB:	61	Gaps:	3

US-10-780-703-2 (1-379) x US-10-780-703-3 (1-2606)

Qy	1	MetAlaIleValSerSerThrThrSerIleIleProMetSerAsnGlnValAsnAsnAsn	20
Db	1	ATGGCAATTGTATCCTCCACAACAAGCATCATTCCCATGAGTAACCAAGTCAACAATAAC	60
Qy	21	GluLysGlyIleGluAspAsnAspHisArgGlyGlyGlnGluSerHisValGlnAsnGlu	40
Db	61	GAAAAAGGTATAGAAGACAATGATCATAGAGGCGCCAAGAGAGTCATGTCCAAAATGAA	120
Qy	41	AspGluAlaAspAspHisAspHisAspMetValMetProGlyPheArgPheHisProThr	60
Db	121	GATGAAGCTGATGATCATGATCATGACATGGTCATGCCCGGATTTAGATTCCATCCTACC	180
Qy	61	GluGluGluLeuIleGluPheTyrLeuArgArgLysValGluGlyLysArgPheAsnVal	80
Db	181	GAAGAAGAACTCATAGAGTTTACCTTCGCCGAAAAGTTGAAGGCAAACGCTTTAATGTA	240
Qy	81	GluLeuIleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro-----	97
Db	241	GAAGTCATCACTTTCTCTCGATCTTTATCGCTATGATCCTTGGGAAGTTCTTGGTAAATAT	300
Qy	97	-----	97

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Db      301 ACATTACATAAACACACATAAATCATCTCAAACCTATTTGGAAATCTTAATTTCTATTCA 360
Qy      97 ----- 97

Db      361 TATGTTAAGATCTTTCTTCTCTCTTATCACTTTCTCTCTCTATTTCTTTTTTTTAACT 420
Qy      97 ----- 97

Db      421 ATATATGTACCTACCTCCTTATGAAGTATTACTATGTCGATCGTTAAACAATTCTCAATAT 480
Qy      97 ----- 97

Db      481 CTTTAAACGCTTCTCCCTCTTTAGTTTCTTTCTTAAATTAACCTAATTAAACAACCTACA 540
Qy      97 ----- 97

Db      541 TATATATCATAAGATATACAAATATGTGTATGTTTTTCATAATTAGCTTATGTATGTTTAA 600
Qy      98 -----AlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyr 110
          |||||||||||||||||||||||||||||||||||||||
Db      601 TCATAGATATATGTATATGCAGCTATGGCGGCGATAGGAGAGAAAGAGTGGTACTTCTAT 660
Qy      111 ValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGly 130
          |||||||||||||||||||||||||||||||||||||||
Db      661 GTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGA 720
Qy      131 TyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGly 150
          |||||||||||||||||||||||||||||||||||||||
Db      721 TATTGGAAAGCCACCGGAGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGA 780
Qy      151 LeuLysLysThrLeuValPheTyrSerGlyLysAlaProLysGlyThrArgThrSerTrp 170
          |||||||||||||||||||||||||||||||||||||||
Db      781 TTAAAGAAAACCTAGTTTTCTACTCTGGTAAAGCCCCCTAAAGGCACTCGTACTAGTTGG 840
Qy      171 IleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLysAla----- 188
          |||||||||||||||||||||||||||||||||||||||
Db      841 ATCATGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGT-ATAAAT 899
          |||||||||||||||||||||||||||||||||||||||
Qy      188 ----- 188
          892-894
Db      900 TCTACTATAACTCTATATATATCCTATTACATACATAGATATAACCCTAGCTAGGTG 959
Qy      188 ----- 188

Db      960 GTGAGGCCCTTTAAAATTGAAATTAATCCCTAGACAGTTTGAATTTTTTCTTTTTTGACTA 1019
Qy      188 ----- 188

Db      1020 GTTTTATTTATTTATTTTGAATTGATTCGATAAGATCAAAAATACTTGTGAATGGACTA 1079
Qy      188 ----- 188

Db      1080 AATGTCAGGCGGCGTTTGCCTTAAATCCAGAAAAATGTTTCATGTCATATGCGTGAACTC 1139
Qy      188 ----- 188

Db      1140 TTTAAATTGCTAGACATGGCCCATATGTTATAGTAGAATACATTAATAGATAGATGCATA 1199
Qy      188 ----- 188

Db      1200 CACATATATATAAACACACAAGTATCACACTCGACATTCATATACCTTAATTCTGCAGAG 1259

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Qy	188	-----	188
Db	1260	ACATAGTTAGTTTTCTTACAATTTATGACATGAATGTTCTCTGCTCTTCCTCACATTAAT	1319
Qy	188	-----	188
Db	1320	TCATGTCTTCTATTTAAGTTACCCAACATTTTTTGAAATAATTTGGCATATATGAATTAT	1379
Qy	188	-----	188
Db	1380	ACCAACATATTTATATGCGAACATTTAAATCTATACGAATGATAACGGTTTATGGAGTA	1439
Qy	188	-----	188
Db	1440	GACCGAAAAAATATTATGTATACGGAAAATGACAATGGATAGATAAAATACATTTTTTGGG	1499
Qy	188	-----	188
Db	1500	CTCTTTCGACTTATATGTCGTCACCATTTGAAACCATAAAATTTATAAAATTTTCTATGTA	1559
Qy	188	-----	188
Db	1560	TATATATGATATTATGATGTATGCATAAGACAGCTAAAACAACAGGGTTGACATAATTAT	1619
Qy	188	-----	188
Db	1620	CTATGTGTATGTATTGCACATTCACCTGTACTAATAAACTAAAATTACGCAATTAAATA	1679
Qy	188	-----	188
Db	1680	TATAAAAAATAATAAATATAATCATCTTAATTATATTGCATTGTTACGTCATATGATAG	1739
Qy	188	-----	188
Db	1740	TACTCTAAATTTCTTCTAAACGTGCTATCTTTTTTTGCTAATGCTAACTTTACATAGTTT	1799
Qy	188	-----	188
Db	1800	GTGAATCTTCTTTCAAACCATATCTTCGATAAATGATATTTTTCATAGATATTGTTAGT	1859
Qy	188	-----	188
Db	1860	CTATATTTGATAATTTGATATATGTATCAAGTCTCTAATCAATGTGCTCATGTATAATTA	1919
Qy	189	-----GluIleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSer	206
Db	1920	TAGGCTGAAATATCATTGTGCCGAGTGTACAAAAGGCCAGGAGTAGAAGATCATCCATCG	1979
Qy	207	ValProArgSerLeuSerThrArgHisHisAsnHisAsnSerSerThrSerSerArgLeu	226
Db	1980	GTACCACGTTCTCTCTCCACAAGACATCATAACCATAACTCATCGACATCATCCCGTTTA	2039
Qy	227	AlaLeuArgGlnGlnGlnHisHisSerSerSerSerAsnHisSerAspAsnAsnLeuAsn	246
Db	2040	GCCTTAAGACAACAACAACACCATTTCCTCCTCTAATCATTCCGACAACAACCTTAAC	2099
Qy	247	AsnAsnAsnAsnIleAsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySer	266
Db	2100	AACAACAACAACATCAACAATCTCGAGAAGCTCTCCACCGAATATTCCGGCGACGGCAGC	2159

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Qy      267 ThrThrThrThrThrThrAsnSerAsnSerAspValThrIleAlaLeuAlaAsnGlnAsn 286
      |||
Db      2160 ACAACAACAACGACCACAAACAGTAACTCTGACGTTACCATTGCTCTAGCCAATCAAAAC 2219

Qy      287 IleTyrArgProMetProTyrAspThrSerAsnAsnThrLeuIleValSerThrArgAsn 306
      |||
Db      2220 ATATATCGTCCAATGCCTTACGACACAAGCAACAACACATTGATAGTCTCTACGAGAAAT 2279

Qy      307 HisGlnAspAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyrGln 326
      |||
Db      2280 CATCAAGACGATGATGAAACTGCCATTGTTGACGATCTTCAAAGACTAGTTAACTACCAA 2339

Qy      327 IleSerAspGly----- 330
      |||
Db      2340 ATATCAGATGGAGGTAACATCAATCACCAATACTTTCAAATTGCTCAACAGTTTCATCAT 2399

Qy      331 -----Ala 331
      |||
Db      2400 ACTCAACAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCGGCGACTACAGCG 2459

Qy      332 ThrThrLeuMetProGlnThrGlnAlaAlaLeuAlaMetAsnMetIleProAlaGlyThr 351
      |||
Db      2460 ACAACGCTAATGCCTCAAACCTCAAGCGGCGTTAGCTATGAACATGATTCTCTGCAGGAACG 2519

Qy      352 IleProAsnAsnAlaLeuTrpAspMetTrpAsnProIleValProAspGlyAsnArgAsp 371
      |||
Db      2520 ATTCCAAACAATGCTTTGTGGGATATGTGGAATCCAATAGTACCAGATGGAAACAGAGAT 2579

Qy      372 HisTyrThrAsnIleProPheLys 379
      |||
Db      2580 CACTATACTAATATTCCTTTTAAG 2603
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